



54600-8130.US00-SEQLIST.TXT

SEQUENCE LISTING

<110> Lim, Moon Young
Edwards, Cynthia A.
Fry, Kirk E.
Bruice, Thomas W.
Starr, Douglas B.
Laurance, Megan E.
Kwok, Yan

<120> DNA Binding Compound-Mediated Molecular
Switch System

<130> 4600-0130.30

<140> US 09/518,297

<141> 2000-03-03

<150> US 60/122,513

<151> 1999-03-03

<150> US 60/154,605

<151> 1999-09-17

<160> 77

<170> FastSEQ for Windows Version 4.0

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<400> 1

cgttcgact t

11

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cggagtactg tcctccg

17

<210> 3

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<221> misc_feature

<222> (1)...(12)

<223> n = A,T,C or G

<400> 3
taattanggg ng

<210> 4
<211> 551
<212> PRT
<213> Homo sapiens

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<222> (0)...(0)
<223> transcriptional regulatory protein

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1 5 10 15
Ser Gly Pro Tyr Val Glu Ile Ile Glu Gln Pro Lys Gln Arg Gly Met
20 25 30
Arg Phe Arg Tyr Lys Cys Glu Gly Arg Ser Ala Gly Ser Ile Pro Gly
35 40 45
Glu Arg Ser Thr Asp Thr Thr Lys Thr His Pro Thr Ile Lys Ile Asn
50 55 60
Gly Tyr Thr Gly Pro Gly Thr Val Arg Ile Ser Leu Val Thr Lys Asp
65 70 75 80
Pro Pro His Arg Pro His Pro His Glu Leu Val Gly Lys Asp Cys Arg
85 90 95
Asp Gly Phe Tyr Glu Ala Glu Leu Cys Pro Asp Arg Cys Ile His Ser
100 105 110
Phe Gln Asn Leu Gly Ile Gln Cys Val Lys Lys Arg Asp Leu Glu Gln
115 120 125
Ala Ile Ser Gln Arg Ile Gln Thr Asn Asn Asn Pro Phe Gln Val Pro
130 135 140
Ile Glu Glu Gln Arg Gly Asp Tyr Asp Leu Asn Ala Val Arg Leu Cys
145 150 155 160
Phe Gln Val Thr Val Arg Asp Pro Ser Gly Arg Pro Leu Arg Leu Pro
165 170 175
Pro Val Leu Pro His Pro Ile Phe Asp Asn Arg Ala Pro Asn Thr Ala
180 185 190
Glu Leu Lys Ile Cys Arg Val Asn Arg Asn Ser Gly Ser Cys Leu Gly
195 200 205
Gly Asp Glu Ile Phe Leu Leu Cys Asp Lys Val Gln Lys Glu Asp Ile
210 215 220
Glu Val Tyr Phe Thr Gly Pro Gly Trp Glu Ala Arg Gly Ser Phe Ser
225 230 235 240
Gln Ala Asp Val His Arg Gln Val Ala Ile Val Phe Arg Thr Pro Pro
245 250 255
Tyr Ala Asp Pro Ser Leu Gln Ala Pro Val Arg Val Ser Met Gln Leu
260 265 270
Arg Arg Pro Ser Asp Arg Glu Leu Ser Glu Pro Met Glu Phe Gln Tyr
275 280 285
Leu Pro Asp Thr Asp Asp Arg His Arg Ile Glu Glu Lys Arg Lys Arg
290 295 300
Thr Tyr Glu Thr Phe Lys Ser Ile Met Lys Lys Ser Pro Phe Ser Gly
305 310 315 320
Pro Thr Asp Pro Arg Pro Pro Pro Arg Arg Ile Ala Val Pro Ser Arg
325 330 335
Ser Ser Ala Ser Val Pro Lys Pro Ala Pro Gln Pro Tyr Pro Phe Thr
340 345 350
Ser Ser Leu Ser Thr Ile Asn Tyr Asp Glu Phe Pro Thr Met Val Phe
355 360 365
Pro Ser Gly Gln Ile Ser Gln Ala Ser Ala Leu Ala Pro Ala Pro Pro
370 375 380

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Gln Val Leu Pro Gln Ala Pro Ala Pro Ala Pro Ala Met Val
 385 390 395 400
 Ser Ala Leu Ala Gln Ala Pro Ala Pro Val Pro Val Leu Ala Pro Gly
 405 410 415
 Pro Pro Gln Ala Val Ala Pro Pro Ala Pro Lys Pro Thr Gln Ala Gly
 420 425 430
 Glu Gly Thr Leu Ser Glu Ala Leu Leu Gln Leu Gln Phe Asp Asp Glu
 435 440 445
 Asp Leu Gly Ala Leu Leu Gly Asn Ser Thr Asp Pro Ala Val Phe Thr
 450 455 460
 Asp Leu Ala Ser Val Asp Asn Ser Glu Phe Gln Gln Leu Leu Asn Gln
 465 470 475 480
 Gly Ile Pro Val Ala Pro His Thr Thr Glu Pro Met Leu Met Glu Tyr
 485 490 495
 Pro Glu Ala Ile Thr Arg Leu Val Thr Gly Ala Gln Arg Pro Pro Asp
 500 505 510
 Pro Ala Pro Ala Pro Leu Gly Ala Pro Gly Leu Pro Asn Gly Leu Leu
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 530 535 540
 Leu Leu Ser Gln Ile Ser Ser
 545 550

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<220>
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<400> 5
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19

<210> 6
 <211> 22
 <212> DNA
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<400> 6
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22

<210> 7
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 <223> n = A,T,C or G

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 <222> (12)...(12)

<223> n = A or C

<400> 7

rgntcantga cny

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<210> 8

<211> 77

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<223> activator sequence

<400> 8

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          20          25          30
Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr Pro His
          35          40          45
Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Phe Glu
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Gln Met Phe Thr Asp Ala Leu Gly Ile Asp Glu Tyr Gly
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<223> repressor sequence

<400> 10

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Lys Asp Val Phe Val Asp Phe Thr Arg Glu Glu Trp Lys Leu Leu Asp
          20          25          30
Thr Ala Gln Gln Ile Val Tyr Arg Asn Val Met Leu Glu Asn Tyr Lys
          35          40          45
Asn Leu Val Ser Leu Gly Tyr Gln Leu Thr Lys Pro Asp Val Ile Leu
          50          55          60
Arg Leu Glu Lys Gly Glu Glu Pro Trp Leu Val Glu Arg Glu Ile His
65          70          75          80
Gln Glu Thr His Pro Asp Ser Glu Thr Ala Phe Glu Ile Lys Ser Ser
          85          90          95
Val

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 <213> Artificial Sequence

<220>
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 Met Ala Ala Val Arg Met Asn Ile Gln Met Leu Leu Glu Ala Ala
 1 5 10 15
 Asp Tyr Leu Glu Arg Arg Glu Arg Glu Ala Glu His Gly Tyr Ala Ser
 20 25 30
 Met Leu Pro Tyr
 35

<210> 12
 <211> 116
 <212> DNA
 <213> Escherichia coli

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> partial promoter sequence

<400> 12
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 gccaccactg acacggaaca acggcaaaca cgccgccggg tcagcggggt tctcct 116

<210> 13
 <211> 22
 <212> DNA
 <213> Escherichia coli

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> partial promoter sequence

<400> 13
 agaaaattat tttaaatttc ct 22

<210> 14
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> modified promoter sequence

<400> 14
 gactgcagtg gtacctagga gg 22

<210> 15
 <211> 22
 <212> DNA
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<210> 16 <211> 22 <212> DNA <213> Artificial Sequence	
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<210> 18 <211> 11 <212> DNA <213> Artificial Sequence	
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 <223> engineered DNA response element

 <400> 22
 cttaaaaata ac 12

 <210> 23
 <211> 16
 <212> DNA
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 <220>
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 <400> 23
 ttgaaaaatc aacgct 16

 <210> 24
 <211> 21
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 <400> 24
 tttttgttcg cacttttttt t 21

 <210> 25
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 <400> 25
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 <210> 26
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 <400> 26
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<211> 6
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 <223> tissue-specific transcription factor

 <400> 27
 acttta 6

 <210> 28
 <211> 9
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 <400> 28
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 <210> 29
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 <400> 29
 gggactttcc 10

 <210> 30
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 <220>
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 gggattttcc 10

 <210> 31
 <211> 50
 <212> DNA
 <213> Artificial Sequence

 <220>
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> engineered DNA response element

<400> 34
 aaaaaattgt gagcgctcac aatttttt 28

<210> 35
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<220>
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<400> 35
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<210> 36
 <211> 10
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> engineered DNA response element

<400> 36
 tctgggatcc 10

<210> 37
 <211> 14
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> engineered DNA response element

<400> 37
 gagttttttt taag 14

<210> 38
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 <212> DNA
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<220>

<223> engineered DNA response element

<400> 38

gagttttaaa agag

14

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<211> 969

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<213> Homo sapiens

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<222> (0)...(0)

<223> transcriptional regulatory protein

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 20 25 30
 Pro Gln Met Ala Leu Pro Thr Ala Asp Gly Pro Tyr Leu Gln Ile Leu
 35 40 45
 Glu Gln Pro Lys Gln Arg Gly Phe Arg Phe Arg Tyr Val Cys Glu Gly
 50 55 60
 Pro Ser His Gly Gly Leu Pro Gly Ala Ser Ser Glu Lys Asn Lys Lys
 65 70 75 80
 Ser Tyr Pro Gln Val Lys Ile Cys Asn Tyr Val Gly Pro Ala Lys Val
 85 90 95
 Ile Val Gln Leu Val Thr Asn Gly Lys Asn Ile His Leu His Ala His
 100 105 110
 Ser Leu Val Gly Lys His Cys Glu Asp Gly Ile Cys Thr Val Thr Ala
 115 120 125
 Gly Pro Lys Asp Met Val Val Gly Phe Ala Asn Leu Gly Ile Leu His
 130 135 140
 Val Thr Lys Lys Lys Val Phe Glu Thr Leu Glu Ala Arg Met Thr Glu
 145 150 155 160
 Ala Cys Ile Arg Gly Tyr Asn Pro Gly Leu Leu Val His Pro Asp Leu
 165 170 175
 Ala Tyr Leu Gln Ala Glu Gly Gly Gly Asp Arg Gln Leu Gly Asp Arg
 180 185 190
 Glu Lys Glu Leu Ile Arg Gln Ala Ala Leu Gln Gln Thr Lys Glu Met
 195 200 205
 Asp Leu Ser Val Val Arg Leu Met Phe Thr Ala Phe Leu Pro Asp Ser
 210 215 220
 Thr Gly Ser Phe Thr Arg Arg Leu Glu Pro Val Val Ser Asp Ala Ile
 225 230 235 240
 Tyr Asp Ser Lys Ala Pro Asn Ala Ser Asn Leu Lys Ile Val Arg Met
 245 250 255
 Asp Arg Thr Ala Gly Cys Val Thr Gly Gly Glu Glu Ile Tyr Leu Leu
 260 265 270
 Cys Asp Lys Val Gln Lys Asp Asp Ile Gln Ile Arg Phe Tyr Glu Glu
 275 280 285
 Glu Glu Asn Gly Gly Val Trp Glu Gly Phe Gly Asp Phe Ser Pro Thr
 290 295 300
 Asp Val His Arg Gln Phe Ala Ile Val Phe Lys Thr Pro Lys Tyr Lys
 305 310 315 320
 Asp Ile Asn Ile Thr Lys Pro Ala Ser Val Phe Val Gln Leu Arg Arg
 325 330 335
 Lys Ser Asp Leu Glu Thr Ser Glu Pro Lys Pro Phe Leu Tyr Tyr Pro
 340 345 350
 Glu Ile Lys Asp Lys Glu Glu Val Gln Arg Lys Arg Gln Lys Leu Met
 355 360 365
 Pro Asn Phe Ser Asp Ser Phe Gly Gly Gly Ser Gly Ala Gly Ala Gly

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370						375					380				
Gly 385	Gly	Gly	Met	Phe	Gly 390	Ser	Gly	Gly	Gly	Gly 395	Gly	Gly	Thr	Gly	Ser 400
Thr	Gly	Pro	Gly	Tyr 405	Ser	Phe	Pro	His	Tyr 410	Gly	Phe	Pro	Thr	Tyr 415	Gly
Gly	Ile	Thr	Phe 420	His	Pro	Gly	Thr	Thr 425	Lys	Ser	Asn	Ala	Gly 430	Met	Lys
His	Gly	Thr 435	Met	Asp	Thr	Glu	Ser 440	Lys	Lys	Asp	Pro	Glu 445	Gly	Cys	Asp
Lys	Ser 450	Asp	Asp	Lys	Asn	Thr 455	Val	Asn	Leu	Phe	Gly 460	Lys	Val	Ile	Glu
Thr 465	Thr	Glu	Gln	Asp	Gln 470	Glu	Pro	Ser	Glu	Ala 475	Thr	Val	Gly	Asn	Gly 480
Glu	Val	Thr	Leu	Thr 485	Tyr	Ala	Thr	Gly	Thr 490	Lys	Glu	Glu	Ser	Ala 495	Gly
Val	Gln	Asp	Asn 500	Leu	Phe	Leu	Glu	Lys 505	Ala	Met	Gln	Leu	Ala 510	Lys	Arg
His	Ala	Asn 515	Ala	Leu	Phe	Asp	Tyr 520	Ala	Val	Thr	Gly	Asp 525	Val	Lys	Met
Leu	Leu 530	Ala	Val	Gln	Arg	His 535	Leu	Thr	Ala	Val	Gln 540	Asp	Glu	Asn	Gly
Asp 545	Ser	Val	Leu	His	Leu 550	Ala	Ile	Ile	His	Leu 555	His	Ser	Gln	Leu	Val 560
Arg	Asp	Leu	Leu	Glu 565	Val	Thr	Ser	Gly	Leu 570	Ile	Ser	Asp	Asp	Ile 575	Ile
Asn	Met	Arg	Asn 580	Asp	Leu	Tyr	Gln	Thr 585	Pro	Leu	His	Leu	Ala 590	Val	Ile
Thr	Lys	Gln 595	Glu	Asp	Val	Val	Glu 600	Asp	Leu	Leu	Arg	Ala 605	Gly	Ala	Asp
Leu	Ser 610	Leu	Leu	Asp	Arg	Leu 615	Gly	Asn	Ser	Val	Leu 620	His	Leu	Ala	Ala
Lys 625	Glu	Gly	His	Asp	Lys 630	Val	Leu	Ser	Ile	Leu 635	Leu	Lys	His	Lys	Lys 640
Ala	Ala	Leu	Leu	Leu 645	Asp	His	Pro	Asn	Gly 650	Asp	Gly	Leu	Asn	Ala 655	Ile
His	Leu	Ala	Met 660	Met	Ser	Asn	Ser	Leu 665	Pro	Cys	Leu	Leu	Leu 670	Leu	Val
Ala	Ala	Gly 675	Ala	Asp	Val	Asn	Ala 680	Gln	Glu	Gln	Lys	Ser 685	Gly	Arg	Thr
Ala	Leu 690	His	Leu	Ala	Val	Glu 695	His	Asp	Asn	Ile	Ser 700	Leu	Ala	Gly	Cys
Leu 705	Leu	Leu	Glu	Gly	Asp 710	Ala	His	Val	Asp	Ser 715	Thr	Thr	Tyr	Asp	Gly 720
Thr	Thr	Pro	Leu	His 725	Ile	Ala	Ala	Gly	Arg 730	Gly	Ser	Thr	Arg	Leu 735	Ala
Ala	Leu	Leu	Lys 740	Ala	Ala	Gly	Ala	Asp 745	Pro	Leu	Val	Glu	Asn 750	Phe	Glu
Pro	Leu	Tyr 755	Asp	Leu	Asp	Asp	Ser 760	Trp	Glu	Asn	Ala	Gly 765	Glu	Asp	Glu
Gly	Val 770	Val	Pro	Gly	Thr	Thr 775	Pro	Leu	Asp	Met	Ala 780	Thr	Ser	Trp	Gln
Val 785	Phe	Asp	Ile	Leu	Asn 790	Gly	Lys	Pro	Tyr	Glu 795	Pro	Glu	Phe	Thr	Ser 800
Asp	Asp	Leu	Leu	Ala 805	Gln	Gly	Asp	Met	Lys 810	Gln	Leu	Ala	Glu	Asp	Val 815
Lys	Leu	Gln 820	Leu	Tyr	Lys	Leu	Leu	Glu 825	Ile	Pro	Asp	Pro	Asp	Lys	Asn
Trp	Ala	Thr 835	Leu	Ala	Gln	Lys	Leu 840	Gly	Leu	Gly	Ile	Leu 845	Asn	Asn	Ala
Phe	Arg 850	Leu	Ser	Pro	Ala	Pro 855	Ser	Lys	Thr	Leu	Met 860	Asp	Asn	Tyr	Glu
Val 865	Ser	Gly	Gly	Thr	Val 870	Arg	Glu	Leu	Val	Glu 875	Ala	Leu	Arg	Gln	Met 880

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Gly Tyr Thr Glu Ala Ile Glu Val Ile Gln Ala Ala Ser Ser Pro Val
 885 890 895
 Lys Thr Thr Ser Gln Ala His Ser Leu Pro Leu Ser Pro Ala Ser Thr
 900 905 910
 Arg Gln Gln Ile Asp Glu Leu Arg Asp Ser Asp Ser Val Cys Asp Thr
 915 920 925
 Gly Val Glu Thr Ser Phe Arg Lys Leu Ser Phe Thr Glu Ser Leu Thr
 930 935 940
 Ser Gly Ala Ser Leu Leu Thr Leu Asn Lys Met Pro His Asp Tyr Gly
 945 950 955 960
 Gln Glu Gly Pro Leu Glu Gly Lys Ile
 965

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<211> 96

<212> DNA

<213> Artificial Sequence

<220>

<223> engineered regulatory sequence

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 agcagagctc gtttagtgaa ccgtcagatc agatct

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96

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 cagagctcgt ttagtgaacc gtcagatcag atct

60

120

154

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<211> 212

<212> DNA

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<220>

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<400> 42

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 tagcgcctaa attgggattt tccaaaaagc cgaaattggg attttccaaa aaccgccgat
 cgcccgcccc gttgacgcaa atgggcggtg ggcgtgtacg gtgggaggtt tatataagca
 gagctcgttt agtgaaccgt cagatcagat ct

60

120

180

212

<210> 43

<211> 96

<212> DNA

<213> Artificial Sequence

<220>

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<400> 43

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60

96

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 atcgcccgcc ccgttgacgc aaatgggcgg taggcgtgta cgggtgggagg cctatataag 120
 cagagctcgt ttagtgaacc gtcagatcag atct 154

<210> 45
 <211> 154
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 45
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 atcgcccgcc ccgttgacgc aaatgggcgg taggcgtgta cgggtgggagg cctatataag 120
 cagagctcgt ttagtgaacc gtcagatcag atct 154

<210> 46
 <211> 762
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> engineered promoter construct

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 tggctattgg ccattgcata cgttgatctc atatcataat atgtacattt atattggctc 120
 atgtccaata tgaccgccat gttggcattg attattgact agttattaat agtaatcaat 180
 tacgggggtca ttagttcata gcccatatat ggagttccgc gttacataac ttacggtaaa 240
 tggcccgctt ggctgaccgc ccaacgaccc ccgcccattg acgtcaataa tgacgtatgt 300
 tcccatagta acgcaaatag ggattttcca ttaacgtcaa tgggtggagt atttacggta 360
 aactgcccac ttggcagtac atcaagtgtg tcatatgcca agtccgcccc ctattgacgt 420
 caatgacggt aaatggcccc cctggcatta tgcccagtac atgactttat gggattttcc 480
 tatttggcag tacatctacg tattagtcac cgctattacc atggtgatgc ggttttggca 540
 gtacaccaat gggcggtgat agcggtttga ctacacgggga tttccaagtc tccaccccat 600
 tgacgtcaat gggagtttgt tttggcacca aggtaaaagg gattttccaa aatgtcgtaa 660
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 tatataagca gagctcgttt agtgaaccgt cagatcaagc tt 762

<210> 47
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 <212> DNA
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<220>
 <223> engineered promoter construct

<400> 47
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 atgtccaata tgaccgccat gttggcattg attattgact agttattaat agtaatcaat 180
 tacgggggtca ttagttcata gcccatatat ggagttccgc gttacataac ttacggtaaa 240

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tgccccgcct	ggctgaccgc	ccaacgaccc	ccgcccattg	acgtcaataa	tgacgtatgt	300
tcccatagta	acgcaaata	tcccgggaaa	ttaacgtcaa	tgggtggagt	atttacggta	360
aactgcccac	ttggcagtac	atcaagtgt	tcatatgcc	agtccgcccc	ctattgacgt	420
caatgacggt	aaatggcccc	cctggcatta	tgcccagtac	atgactttat	tctcgaggaa	480
tatttggcag	tacatctacg	tattagtc	cgctattacc	atgggtgatgc	ggttttggca	540
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